

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 09/060,294B  
Source: 1FW/6  
Date Processed by STIC: 1/3/05

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 01/03/2005

PATENT APPLICATION: US/09/060,294B

TIME: 16:38:44

Input Set : A:\US09060294.txt

Output Set: N:\CRF4\01032005\I060294B.raw

## SEQUENCE LISTING

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4 (1) GENERAL INFORMATION:
6   (i) APPLICANT: Martin Roland Jensen
7           Soren Mouritsen
8           Henrik Elsner
9           Iben Dalum
11  (ii) TITLE OF INVENTION: Modified human TNF-alpha molecules, DNA
12                        encoding them, and vaccines containing said modified
13                        TNF-alpha or DNA
15  (iii) NUMBER OF SEQUENCES: 44
17  (iv) CORRESPONDENCE ADDRESS:
18      (A) ADDRESSEE: JACOBSON HOLMAN, PLLC
19      (B) STREET: 400 Seventh St., N.W.
20      (C) CITY: Washington
21      (D) STATE: DC
22      (E) COUNTRY: USA
C--> 23      (F) ZIP: 20004
25  (v) COMPUTER READABLE FORM:
26      (A) MEDIUM TYPE: Floppy disk
27      (B) COMPUTER: IBM PC compatible
28      (C) OPERATING SYSTEM: PC-DOS/MS-DOS
29      (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
31  (vi) CURRENT APPLICATION DATA:
C--> 32      (A) APPLICATION NUMBER: US/09/060,294B
C--> 33      (B) FILING DATE: 15-Apr-1998
35  (vii) PRIOR APPLICATION DATA:
36      (A) APPLICATION NUMBER: 60/044,187
37      (B) FILING DATE: 24-APR-1997
39  (viii) ATTORNEY/AGENT INFORMATION:
40      (A) NAME: William E. Player
41      (B) REGISTRATION NUMBER: 31,409
42      (C) REFERENCE/DOCKET NUMBER: P60953US1
44  (ix) TELECOMMUNICATION INFORMATION:
45      (A) TELEPHONE: (202) 638-6666
46      (B) TELEFAX: (202) 393-5350
48 (2) INFORMATION FOR SEQ ID NO: 1:
50   (i) SEQUENCE CHARACTERISTICS:
51      (A) LENGTH: 474 base pairs
52      (B) TYPE: nucleic acid
53      (C) STRANDEDNESS: double
54      (D) TOPOLOGY: linear
56   (ii) MOLECULE TYPE: cDNA
58   (iii) HYPOTHETICAL: NO

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60      (iv) ANTI-SENSE: NO
62      (vi) ORIGINAL SOURCE:
63          (A) ORGANISM: Homo sapiens
65      (ix) FEATURE:
66          (A) NAME/KEY: CDS
67          (B) LOCATION:1..474
68          (C) IDENTIFICATION METHOD: experimental
69          (D) OTHER INFORMATION:/codon_start= 1
70 /function= "Antigen"
71 /product= "TNF-alpha analog"
72 /evidence= EXPERIMENTAL
73 /gene= "tnfp2-1"
74 /standard_name= "TNF2-1"
76      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
78 ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT CAG TAC ATT AAA GCC AAT      48
79 Met Val Arg Ser Ser Ser Arg Thr Pro Ser Gln Tyr Ile Lys Ala Asn
80   1          5          10          15
82 TCT AAA TTC ATC GGT ATA ACT GAG CTG CAG CTC CAG TGG CTG AAC CGC      96
83 Ser Lys Phe Ile Gly Ile Thr Glu Leu Gln Leu Gln Trp Leu Asn Arg
84          20          25          30
86 CGG GCC AAT GCC CTC CTG GCC AAT GGC GTG GAG CTG AGA GAT AAC CAG      144
87 Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
88          35          40          45
90 CTG GTG GTG CCA TCA GAG GGC CTG TAC CTC ATC TAC TCC CAG GTC CTC      192
91 Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
92          50          55          60
94 TTC AAG GGC CAA GGC TGC CCC TCC ACC CAT GTG CTC CTC ACC CAC ACC      240
95 Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
96          65          70          75          80
98 ATC AGC CGC ATC GCC GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT      288
99 Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
100          85          90          95
102 GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC      336
103 Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
104          100          105          110
106 AAG CCC TGG TAT GAG CCC ATC TAT CTG GGA GGG GTC TTC CAG CTG GAG      384
107 Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
108          115          120          125
110 AAG GGT GAC CGA CTC AGC GCT GAG ATC AAT CGG CCC GAC TAT CTC GAC      432
111 Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
112          130          135          140
114 TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC      474
115 Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
116 145          150          155

119 (2) INFORMATION FOR SEQ ID NO: 2:
121      (i) SEQUENCE CHARACTERISTICS:
122          (A) LENGTH: 158 amino acids
123          (B) TYPE: amino acid
124          (D) TOPOLOGY: linear

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126 (ii) MOLECULE TYPE: protein  
 128 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 130 Met Val Arg Ser Ser Ser Arg Thr Pro Ser Gln Tyr Ile Lys Ala Asn  
 131 1 5 10 15  
 133 Ser Lys Phe Ile Gly Ile Thr Glu Leu Gln Leu Gln Trp Leu Asn Arg  
 134 20 25 30  
 136 Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln  
 137 35 40 45  
 139 Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu  
 140 50 55 60  
 142 Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr  
 143 65 70 75 80  
 145 Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser  
 146 85 90 95  
 148 Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala  
 149 100 105 110  
 151 Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu  
 152 115 120 125  
 154 Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp  
 155 130 135 140  
 157 Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu  
 158 145 150 155

161 (2) INFORMATION FOR SEQ ID NO: 3:

163 (i) SEQUENCE CHARACTERISTICS:

164 (A) LENGTH: 474 base pairs

165 (B) TYPE: nucleic acid

166 (C) STRANDEDNESS: double

167 (D) TOPOLOGY: linear

169 (ii) MOLECULE TYPE: DNA (genomic)

171 (iii) HYPOTHETICAL: NO

173 (iv) ANTI-SENSE: NO

175 (vi) ORIGINAL SOURCE:

176 (A) ORGANISM: Homo sapiens

178 (ix) FEATURE:

179 (A) NAME/KEY: CDS

180 (B) LOCATION:1..474

181 (D) OTHER INFORMATION:/codon\_start= 1

182 /function= "Antigen"

183 /product= "TNF-alpha analog"

184 /gene= "tnfp2-3"

185 /standard\_name= "TNF2-3"

187 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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 190 Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His  
 W--> 191 160 165 170 175  
 193 GTT GTA GCA AAC CCT CAA GCT GAG GGG CAG CTC CAG TGG CTG AAC CGC 96  
 194 Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg  
 W--> 195 180 185 190  
 197 CGG GCC AAT GCC CTC CTG GCC AAT GGC GTG GAG CTG AGA GAT AAC CAG 144

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198 Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
W--> 199          195          200          205
201 CTG GTG GTG CCA TCA GAG GGC CTG TAC CTC ATC TAC TCC CAG GTC CTC      192
202 Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
W--> 203          210          215          220
205 TTC CAG TAC ATA AAG GCC AAC TCC AAG TTT ATC GGC ATC ACC GAG CTC      240
206 Phe Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
W--> 207          225          230          235
209 ATC AGC CGC ATC GCC GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT      288
210 Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
W--> 211 240          245          250          255
213 GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC      336
214 Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
W--> 215          260          265          270
217 AAG CCC TGG TAT GAG CCC ATC TAT CTG GGA GGG GTC TTC CAG CTG GAG      384
218 Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
W--> 219          275          280          285
221 AAG GGT GAC CGA CTC AGC GCT GAG ATC AAT CGG CCC GAC TAT CTC GAC      432
222 Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
W--> 223          290          295          300
225 TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC      474
226 Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
W--> 227          305          310          315
230 (2) INFORMATION FOR SEQ ID NO: 4:
232 (i) SEQUENCE CHARACTERISTICS:
233 (A) LENGTH: 158 amino acids
234 (B) TYPE: amino acid
235 (D) TOPOLOGY: linear
237 (ii) MOLECULE TYPE: protein
239 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
241 Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
242 1          5          10          15
244 Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
245          20          25          30
247 Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
248          35          40          45
250 Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
251          50          55          60
253 Phe Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
254 65          70          75          80
256 Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
257          85          90          95
259 Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
260          100          105          110
262 Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
263          115          120          125
265 Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
266          130          135          140
268 Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu

```

## RAW SEQUENCE LISTING

DATE: 01/03/2005

PATENT APPLICATION: US/09/060,294B

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Input Set : A:\US09060294.txt

Output Set: N:\CRF4\01032005\I060294B.raw

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269 145                      150                      155
272 (2) INFORMATION FOR SEQ ID NO: 5:
274     (i) SEQUENCE CHARACTERISTICS:
275         (A) LENGTH: 474 base pairs
276         (B) TYPE: nucleic acid
277         (C) STRANDEDNESS: double
278         (D) TOPOLOGY: linear
280     (ii) MOLECULE TYPE: DNA (genomic)
282     (iii) HYPOTHETICAL: NO
284     (iv) ANTI-SENSE: NO
286     (vi) ORIGINAL SOURCE:
287         (A) ORGANISM: Homo sapiens
289     (ix) FEATURE:
290         (A) NAME/KEY: CDS
291         (B) LOCATION:1..474
292         (D) OTHER INFORMATION:/codon_start= 1
293 /function= "Antigen"
294 /product= "TNF-alpha analog"
295 /gene= "tnfp2-4"
296 /standard_name= "TNF2-4"
298     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
300 ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT GAC AAG CCT GTA GCC CAT      48
301 Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
W--> 302 160                      165                      170                      175
304 GTT GTA GCA AAC CCT CAA GCT GAG GGG CAG CTC CAG TGG CTG AAC CGC      96
305 Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
W--> 306                      180                      185                      190
308 CGG GCC AAT GCC CTC CTG GCC AAT GGC GTG GAG CTG AGA GAT AAC CAG      144
309 Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
W--> 310                      195                      200                      205
312 CTG GTG GTG CCA TCA GAG GGC CTG TAC CTC ATC TAC TCC CAG GTC CTC      192
313 Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
W--> 314                      210                      215                      220
316 TTC AAG GGC CAA GGC TGC CCC TCC ACC CAT GTG CTC CTC ACC CAC ACC      240
317 Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
W--> 318                      225                      230                      235
320 ATC AGC CGC ATC GCC GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT      288
321 Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
W--> 322 240                      245                      250                      255
324 GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC      336
325 Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
W--> 326                      260                      265                      270
328 AAG CCC CAG TAT ATC AAG GCC AAT TCG AAA TTC ATC GGC ATC ACG GAG      384
329 Lys Pro Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
W--> 330                      275                      280                      285
332 CTC GGT GAC CGA CTC AGC GCT GAG ATC AAT CGG CCC GAC TAT CTC GAC      432
333 Leu Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
W--> 334                      290                      295                      300
335 TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC      474

```

## VERIFICATION SUMMARY

DATE: 01/03/2005

PATENT APPLICATION: US/09/060,294B

TIME: 16:38:45

Input Set : A:\US09060294.txt

Output Set: N:\CRF4\01032005\I060294B.raw

L:23 M:220 C: Keyword misspelled or invalid format, [(F) ZIP:]  
L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:191 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:195 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:199 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:203 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:207 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:211 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:215 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:219 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:223 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:227 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:302 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:306 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:310 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:314 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:318 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:322 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:326 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:330 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:334 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:337 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:411 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
L:415 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
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L:431 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
L:435 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
L:439 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
L:443 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
L:447 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
L:522 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9  
L:526 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9  
L:530 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9  
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L:633 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
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L:641 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:645 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:649 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11

## VERIFICATION SUMMARY

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PATENT APPLICATION: US/09/060,294B

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Input Set : A:\US09060294.txt

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L:653 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:657 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:661 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:665 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:669 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11